

SEQUENCE LISTING

<110> University of Florida Research Foundation, Inc.
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 Lyerly Linebarger, Carla R.

<120> Heat Stable Variants of Adenosine Diphosphate Glucose Pyrophosphorylase

<130> UF-371XC1 PCT

<150> US 60/496,188
 <151> 2003-08-18

<160> 42

<170> PatentIn version 3.2

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Asp Ser Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
          35          40          45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
          50          55          60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65          70          75          80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
          85          90          95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
          100         105         110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
          115         120         125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
          130         135         140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
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Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
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Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
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 225 230 235 240
 Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
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 Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
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 Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
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 Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp
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20          25          30

Asp Ser Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
35          40          45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
50          55          60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65          70          75          80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
85          90          95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
100         105         110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
115         120         125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
130         135         140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
145         150         155         160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
165         170         175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
180         185         190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
195         200         205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
210         215         220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu
225         230         235         240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
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Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
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20           25           30

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Asp Ser Gln Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
35           40           45

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Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys

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Asp	Ile	Pro	Val	Ser	Asn	Cys	Leu	Asn	Ser	Asn	Ile	Ser	Lys	Ile	Tyr
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Val	Leu	Thr	Gln	Phe	Asn	Ser	Ala	Ser	Leu	Asn	Arg	His	Leu	Ser	Arg
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385	390	395
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Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg		
420	425	430
Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala		
435	440	445
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Asp Ser Gln Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
35        40        45
Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
50        55        60
Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
65        70        75        80
Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
85        90        95
Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
100       105       110
Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
115       120       125
Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
130       135       140
Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn

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		165		170		175
Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr						
		180		185		190
Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu						
		195		200		205
Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro						
		210		215		220
Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly						
225		230		235		240
Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly						
		245		250		255
Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln						
		260		265		270
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Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu						
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Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr						
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Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile						
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Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp						
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Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys						
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Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg						
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Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala						
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Ala Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val						

450	455	460	
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gctgagaaac cgaaaggaga gcagttgaaa gcaatgatgg ttgacaccac catacttggc			720
cttgatgacg tgagggcaaa ggaaatgcct tatattgcta gcatgggtat ctatgttttc			780
agcaaagatg taatgcttca gtcctccgt gaacaatttc ctgaagccaa tgactttgga			840
agtgaggtta ttccaggtgc aaccagcatt ggaaagaggg ttcaggctta tctgtatgat			900
ggttactggg aagatatcgg taccattgcg gcattttata atgcaaactt gggaataacc			960
aagaagccaa taccagattt cagcttctat gaccgttttg ctccaattta tacacaacct			1020
cgacacctgc caccttcaaa ggttcttgat gctgatgtga cagacagtgt tattggtgaa			1080
ggatgtgtta ttaaaaaactg caagataaac cattctgtag ttggactccg atcttgcata			1140
tctgaagggtg ctatcataga ggacagttta ctaatgggtg cggactacta tgagacagaa			1200
gctgataaaa aactccttgc cgaaaaaggt ggcattccta ttggtattgg gaaaaattca			1260
tgcatcagga gagcaatcat tgacaagaat gctcgaattg gagacaatgt taagatactc			1320
aatgctgaca atgttcaaga agctgcaatg gagacagacg ggtacttcat caaagggtgga			1380

attgtcacag tgatcaagga tgctttactc cctagtggaa cagttata

1428

<210> 10
 <211> 476
 <212> PRT
 <213> zea mays

<400> 10

Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Pro Trp Asn Ala
 1 5 10 15

Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
 20 25 30

Asp Ser Glu Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
 35 40 45

Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
 50 55 60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
 65 70 75 80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
 85 90 95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
 100 105 110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
 115 120 125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
 130 135 140

Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn
 145 150 155 160

Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp
 165 170 175

Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr
 180 185 190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu
 195 200 205

Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro
 210 215 220

Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly
 225 230 235 240

Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly

	245		250		255
Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln	260		265		270
Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr	275		280		285
Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu	290		295		300
Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr	305		310		315
Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile		325		330	335
Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp		340		345	350
Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys		355		360	365
Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala		370		375	380
Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu		385		390	395
Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile		405		410	415
Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg		420		425	430
Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala		435		440	445
Ala Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val		450		455	460
Ile Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile		465		470	475

<210> 11

<211> 1582

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

<400> 11

ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
115 120 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
130 135 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
145 150 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
160 165 170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
175 180 185 190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
210 215 220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cat agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser	
320 325 330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc	1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
355 360 365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	
370 375 380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc	1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile	
385 390 395	

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
 Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
 400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
 415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
 435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
 450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
 465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480 485 490

tac tcg tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca 1539
 Tyr Ser Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala
 495 500 505 510

acc atc aac gat ggg tct gtc ata tagatcggt gcgtktgcg 1582
 Thr Ile Asn Asp Gly Ser Val Ile
 515

<210> 12
 <211> 518
 <212> PRT
 <213> Zea mays

<400> 12

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1 5 10 15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175
 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
 195 200 205
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
 210 215 220
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
 225 230 235 240
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
 245 250 255
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
 260 265 270
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
 275 280 285
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
 290 295 300
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
 305 310 315 320
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
 325 330 335
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
 385 390 395 400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser
 485 490 495
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 500 505 510
 Asn Asp Gly Ser Val Ile
 515

<210> 13
 <211> 1582
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (10)..(1563)
 <223> Shrunk-2 gene revertant form, modified to be
 heat stable

<220>
 <221> variation
 <222> (267)
 <223> k = g or t; amino acid 86 = Ala.

<220>
 <221> variation
 <222> (1008)
 <223> y = c or t.

<220>
 <221> variation
 <222> (1368)
 <223> r = a or g; amino acid 453 = Pro.

<220>
 <221> variation
 <222> (1578)
 <223> k = g or t.

<400> 13

ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His

1

5

10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
 65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
 80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
 115 120 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
 130 135 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
 Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
 145 150 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531
 Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
 160 165 170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579
 Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
 175 180 185 190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627
 Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
 195 200 205

gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt 675
 Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu
 210 215 220

gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	
		225					230					235				
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	
	240					245				250						
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggt	gct	gat	819
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	
255				260					265					270		
ttg	aat	tct	atg	aga	gtt	gag	acc	aac	ttc	ctg	agc	tat	gct	ata	gat	867
Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	
			275					280					285			
gat	gca	cag	aaa	tat	cca	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc	915
Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	
		290					295					300				
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta	963
Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	
	305					310					315					
cat	gac	ttt	gga	tct	gaa	atc	ctc	cca	aga	gct	gta	cta	gat	tay	agt	1011
His	Asp	Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Tyr	Ser	
	320				325					330						
gtg	cag	gca	tgc	att	ttt	acg	ggc	tat	tgg	gag	gat	gtt	gga	aca	atc	1059
Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	
335				340				345						350		
aaa	tca	ttc	ttt	gat	gca	aac	ttg	gcc	ctc	act	gag	cag	cct	tcc	aag	1107
Lys	Ser	Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	
			355				360						365			
ttt	gat	ttt	tac	gat	cca	aaa	aca	cct	ttc	ttc	act	gca	ccc	cga	tgc	1155
Phe	Asp	Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys	
		370					375					380				
ttg	cct	ccg	acg	caa	ttg	gac	aag	tgc	aag	atg	aaa	tat	gca	ttt	atc	1203
Leu	Pro	Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Ala	Phe	Ile	
		385				390					395					
tca	gat	ggt	tgc	tta	ctg	aga	gaa	tgc	aac	atc	gag	cat	tct	gtg	att	1251
Ser	Asp	Gly	Cys	Leu	Leu	Arg	Glu	Cys	Asn	Ile	Glu	His	Ser	Val	Ile	
	400				405					410						
gga	gtc	tgc	tca	cgt	gtc	agc	tct	gga	tgt	gaa	ctc	aag	gac	tcc	gtg	1299
Gly	Val	Cys	Ser	Arg	Val	Ser	Ser	Gly	Cys	Glu	Leu	Lys	Asp	Ser	Val	
415				420				425						430		
atg	atg	gga	gcg	gac	atc	tat	gaa	act	gaa	gaa	gaa	gct	tca	aag	cta	1347
Met	Met	Gly	Ala	Asp	Ile	Tyr	Glu	Thr	Glu	Glu	Glu	Ala	Ser	Lys	Leu	
			435				440					445				

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
 450 455 460
 agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
 465 470 475
 atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480 485 490
 tac tcg tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca 1539
 Tyr Ser Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala
 495 500 505 510
 acc atc aac gat ggg tct gtc ata tagatcggct gcgktktgcg 1582
 Thr Ile Asn Asp Gly Ser Val Ile
 515

<210> 14
 <211> 518
 <212> PRT
 <213> Zea mays

<400> 14

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1 5 10 15
 Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
 20 25 30
 Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45
 Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60
 Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95
 Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala

145		150		155		160
Asp Gly Ser Val	Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro					
	165		170		175	
Ala Gly Trp Phe	Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp					
	180		185		190	
Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile						
	195		200		205	
Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln						
	210		215		220	
Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val						
	225		230		235	240
Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr						
	245		250		255	
Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn						
	260		265		270	
Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala						
	275		280		285	
Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys						
	290		295		300	
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp						
	305		310		315	320
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln						
	325		330		335	
Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser						
	340		345		350	
Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp						
	355		360		365	
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro						
	370		375		380	
Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp						
	385		390		395	400
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val						
	405		410		415	
Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met						
	420		425		430	
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu						
	435		440		445	
Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn						

450 455 460
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser
 485 490 495
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 500 505 510
 Asn Asp Gly Ser Val Ile
 515

<210> 15
 <211> 1576
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (10)..(1563)
 <223> Shrunk-2 gene revertant form, modified to be
 heat stable

<220>
 <221> variation
 <222> (267)
 <223> k = g or t; amino acid 86 = Ala.

<220>
 <221> variation
 <222> (1008)
 <223> y = c or t.

<220>
 <221> variation
 <222> (1368)
 <223> r = a or g; amino acid 453 = Pro.

<220>
 <221> variation
 <222> (1578)
 <223> k = g or t.

<400> 15
 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
 1 5 10
 cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30
 agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe

										35											40											45												
ggt	ggt	aga	ggt	gct	gca	act	aca	caa	tgt	att	ctt	acc	tca	gat	gct	195																												
Gly	Gly	Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala																													
										50											55											60												
tgt	cct	gaa	act	ctt	cat	tct	caa	aca	cag	tcc	tct	agg	aaa	aat	tat	243																												
Cys	Pro	Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr																													
										65											70											75												
gct	gat	gca	aac	cgt	gta	tct	gck	atc	att	ttg	ggc	gga	ggc	act	gga	291																												
Ala	Asp	Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly																													
										80											85											90												
tct	cag	ctc	ttt	cct	ctg	aca	agc	aca	aga	gct	acg	cct	gct	gta	cct	339																												
Ser	Gln	Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro																													
										95											100											105											110	
ggt	gga	gga	tgt	tac	agg	ctt	att	gat	atc	cct	atg	agt	aac	tgc	ttc	387																												
Val	Gly	Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe																													
										115											120											125												
aac	agt	ggt	ata	aat	aag	ata	ttt	gtg	atg	agt	cag	ttc	aat	tct	act	435																												
Asn	Ser	Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr																													
										130											135											140												
tcg	ctt	aac	cgc	cat	att	cat	cgt	aca	tac	ctt	gaa	ggc	ggg	atc	aac	483																												
Ser	Leu	Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn																													
										145											150											155												
ttt	gct	gat	gga	tct	gta	cag	gta	tta	gcg	gct	aca	caa	atg	cct	gaa	531																												
Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu																													
										160											165											170												
gag	cca	gct	gga	tgg	ttc	cag	ggt	aca	gca	gac	tct	atc	aga	aaa	ttt	579																												
Glu	Pro	Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe																													
										175											180											185											190	
atc	tgg	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627																												
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile																													
										195											200											205												
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675																												
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu																													
										210											215											220												
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723																												
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala																													
										225											230											235												
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771																												
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp																													
										240											245											250												
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggt	gct	gat	819																												
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp																													

255	260	265	270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat				867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp				
	275	280	285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc				915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe				
	290	295	300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta				963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu				
	305	310	315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt				1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser				
	320	325	330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc				1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile				
	335	340	345	350
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag				1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys				
	355	360	365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc				1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys				
	370	375	380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc				1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile				
	385	390	395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att				1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile				
	400	405	410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg				1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val				
	415	420	425	430
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta				1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu				
	435	440	445	
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata				1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile				
	450	455	460	
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg				1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val				
	465	470	475	
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg				1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly				
	480	485	490	

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgctktgcg 1576
 Asn Asp Gly Ser Val Ile
 515

<210> 16
 <211> 516
 <212> PRT
 <213> Zea mays

<400> 16

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1 5 10 15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
 195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln

210	215	220
Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val		
225	230	235 240
Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr		
	245	250 255
Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn		
	260	265 270
Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala		
	275	280 285
Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys		
	290	295 300
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp		
305	310	315 320
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln		
	325	330 335
Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser		
	340	345 350
Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp		
	355	360 365
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro		
	370	375 380
Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp		
385	390	395 400
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val		
	405	410 415
Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met		
	420	425 430
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu		
	435	440 445
Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn		
	450	455 460
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr		
465	470	475 480
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr		
	485	490 495
Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp		
	500	505 510
Gly Ser Val Ile		

515

<210> 17
 <211> 1576
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (10)..(1563)
 <223> Shrunk-2 gene revertant form, modified to be
 heat stable

<220>
 <221> variation
 <222> (267)
 <223> k = g or t; amino acid 86 = Ala.

<220>
 <221> variation
 <222> (540)
 <223> n = a or g or c or t/u, unknown, or other.

<220>
 <221> variation
 <222> (1008)
 <223> y = c or t.

<220>
 <221> variation
 <222> (1368)
 <223> r = a or g; amino acid 453 = Pro.

<220>
 <221> variation
 <222> (1578)
 <223> k = g or t.

<400> 17
 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
 1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243

Cys	Pro	Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr		
	65						70					75					
gct	gat	gca	aac	cgt	gta	tct	gck	atc	att	ttg	ggc	gga	ggc	act	gga	291	
Ala	Asp	Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly		
	80					85					90						
tct	cag	ctc	ttt	cct	ctg	aca	agc	aca	aga	gct	acg	cct	gct	gta	cct	339	
Ser	Gln	Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro		
	95				100					105					110		
ggt	gga	gga	tgt	tac	agg	ctt	att	gat	atc	cct	atg	agt	aac	tgc	ttc	387	
Val	Gly	Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe		
				115					120					125			
aac	agt	ggt	ata	aat	aag	ata	ttt	gtg	atg	agt	cag	ttc	aat	tct	act	435	
Asn	Ser	Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr		
			130					135					140				
tcg	ctt	aac	cgc	cat	att	cat	cgt	aca	tac	ctt	gaa	ggc	ggg	atc	aac	483	
Ser	Leu	Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn		
		145					150					155					
ttt	gct	gat	gga	tct	gta	cag	gta	tta	gcg	gct	aca	caa	atg	cct	gaa	531	
Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu		
	160					165					170						
gag	cca	ccn	gga	tgg	ttc	cag	ggt	aca	gca	gac	tct	atc	aga	aaa	ttt	579	
Glu	Pro	Pro	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe		
	175				180					185					190		
atc	tgg	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627	
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile		
			195						200					205			
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675	
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu		
			210					215				220					
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723	
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala		
		225					230					235					
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771	
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp		
		240				245					250						
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggt	gct	gat	819	
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp		
	255				260					265					270		
ttg	aat	tct	atg	aga	gtt	gag	acc	aac	ttc	ctg	agc	tat	gct	ata	gat	867	
Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp		
				275					280					285			

gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser	
320 325 330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc	1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
355 360 365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	
370 375 380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc	1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile	
385 390 395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att	1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile	
400 405 410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg	1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val	
415 420 425 430	
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta	1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu	
435 440 445	
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata	1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile	
450 455 460	
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg	1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val	
465 470 475	
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg	1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly	
480 485 490	
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc	1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile	
495 500 505 510	

aac gat ggg tct gtc ata tagatcggct gcgctktgcg
 Asn Asp Gly Ser Val Ile
 515

1576

<210> 18
 <211> 516
 <212> PRT
 <213> Zea mays

<400> 18

Met	Gln	Phe	Ala	Leu	Ala	Leu	Asp	Thr	Asn	Ser	Gly	Pro	His	Gln	Ile	1	5	10	15
Arg	Ser	Cys	Glu	Gly	Asp	Gly	Ile	Asp	Arg	Leu	Glu	Lys	Leu	Ser	Ile	20	25	30	
Gly	Gly	Arg	Lys	Gln	Glu	Lys	Ala	Leu	Arg	Asn	Arg	Cys	Phe	Gly	Gly	35	40	45	
Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala	Cys	Pro	50	55	60	
Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	Ala	Asp	65	70	75	80
Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gln	85	90	95	
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly	100	105	110	
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser	115	120	125	
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu	130	135	140	
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala	145	150	155	160
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro	165	170	175	
Pro	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp	180	185	190	
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile	195	200	205	
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln	210	215	220	
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val	225	230	235	240
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr				

245										250					255				
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn				
			260					265					270						
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala				
		275					280					285							
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys				
	290					295					300								
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp				
305					310					315					320				
Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	His	Ser	Val	Gln				
				325				330						335					
Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser				
			340					345					350						
Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	Phe	Asp				
		355					360					365							
Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys	Leu	Pro				
	370					375					380								
Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Ala	Phe	Ile	Ser	Asp				
385					390					395					400				
Gly	Cys	Leu	Leu	Arg	Glu	Cys	Asn	Ile	Glu	His	Ser	Val	Ile	Gly	Val				
				405					410					415					
Cys	Ser	Arg	Val	Ser	Ser	Gly	Cys	Glu	Leu	Lys	Asp	Ser	Val	Met	Met				
			420					425					430						
Gly	Ala	Asp	Ile	Tyr	Glu	Thr	Glu	Glu	Glu	Ala	Ser	Lys	Leu	Leu	Leu				
		435					440					445							
Ala	Gly	Lys	Val	Pro	Val	Gly	Ile	Gly	Arg	Asn	Thr	Lys	Ile	Arg	Asn				
	450					455						460							
Cys	Ile	Ile	Asp	Met	Asn	Ala	Arg	Ile	Gly	Lys	Asn	Val	Val	Ile	Thr				
465					470					475					480				
Asn	Ser	Lys	Gly	Ile	Gln	Glu	Ala	Asp	His	Pro	Glu	Glu	Gly	Tyr	Tyr				
				485					490					495					
Ile	Arg	Ser	Gly	Ile	Val	Val	Ile	Leu	Lys	Asn	Ala	Thr	Ile	Asn	Asp				
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Gly	Ser	Val	Ile																
		515																	

<210> 19

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1209)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

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<222> (1371)

<223> h = a or c or t/u.

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<221> variation

<222> (1578)

<223> k = g or t.

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ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His

1

5

10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99

Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

15

20

25

30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147

Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe

35

40

45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195

Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala

50

55

60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243

Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr

65	70	75	
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291			
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly	80	85	90
tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339			
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro	95	100	105 110
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387			
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe	115	120	125
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435			
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	130	135	140
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483			
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	145	150	155
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531			
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	160	165	170
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579			
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	175	180	185 190
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627			
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	195	200	205
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt 675			
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	210	215	220
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct 723			
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	225	230	235
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat 771			
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	240	245	250
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat 819			
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	255	260	265 270
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat 867			
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	275	280	285
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc 915			

Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe		
			290					295					300				
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta	963	
Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu		
		305					310					315					
cat	gac	ttt	gga	tct	gaa	atc	ctc	cca	aga	gct	gta	cta	gat	cay	agt	1011	
His	Asp	Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	His	Ser		
	320					325					330						
gtg	cag	gca	tgc	att	ttt	acg	ggc	tat	tgg	gag	gat	gtt	gga	aca	atc	1059	
Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile		
335					340					345					350		
aaa	tca	ttc	ttt	gat	gca	aac	ttg	gcc	ctc	act	gag	cag	cct	tcc	aag	1107	
Lys	Ser	Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys		
				355				360					365				
ttt	gat	ttt	tac	gat	cca	aaa	aca	cct	ttc	ttc	act	gca	ccc	cga	tgc	1155	
Phe	Asp	Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys		
			370					375					380				
ttg	cct	ccg	acg	caa	ttg	gac	aag	tgc	aag	atg	aaa	tat	gca	ttt	atc	1203	
Leu	Pro	Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Ala	Phe	Ile		
		385					390					395					
tca	cay	ggg	tgc	tta	ctg	aga	gaa	tgc	aac	atc	gag	cat	tct	gtg	att	1251	
Ser	His	Gly	Cys	Leu	Leu	Arg	Glu	Cys	Asn	Ile	Glu	His	Ser	Val	Ile		
	400					405					410						
gga	gtc	tgc	tca	cgt	gtc	agc	tct	gga	tgt	gaa	ctc	aag	gac	tcc	gtg	1299	
Gly	Val	Cys	Ser	Arg	Val	Ser	Ser	Gly	Cys	Glu	Leu	Lys	Asp	Ser	Val		
415					420					425					430		
atg	atg	gga	gcg	gac	atc	tat	gaa	act	gaa	gaa	gaa	gct	tca	aag	cta	1347	
Met	Met	Gly	Ala	Asp	Ile	Tyr	Glu	Thr	Glu	Glu	Glu	Ala	Ser	Lys	Leu		
				435					440					445			
ctg	tta	gct	ggg	aag	gtc	ccr	ath	gga	ata	gga	agg	aac	aca	aag	ata	1395	
Leu	Leu	Ala	Gly	Lys	Val	Pro	Ile	Gly	Ile	Gly	Arg	Asn	Thr	Lys	Ile		
			450					455					460				
agg	aac	tgt	atc	att	gac	atg	aat	gct	agg	att	ggg	aag	aac	gtg	gtg	1443	
Arg	Asn	Cys	Ile	Ile	Asp	Met	Asn	Ala	Arg	Ile	Gly	Lys	Asn	Val	Val		
		465					470					475					
atc	aca	aac	agt	aag	ggc	atc	caa	gag	gct	gat	cac	ccg	gaa	gaa	ggg	1491	
Ile	Thr	Asn	Ser	Lys	Gly	Ile	Gln	Glu	Ala	Asp	His	Pro	Glu	Glu	Gly		
	480					485					490						
tac	tac	ata	agg	tct	gga	atc	gtg	gtg	atc	ctg	aag	aat	gca	acc	atc	1539	
Tyr	Tyr	Ile	Arg	Ser	Gly	Ile	Val	Val	Ile	Leu	Lys	Asn	Ala	Thr	Ile		
495					500					505					510		
aac	gat	ggg	tct	gtc	ata	tagatcggct	gcg	tktgcg								1576	

Asn Asp Gly Ser Val Ile
515

<210> 20
<211> 516
<212> PRT
<213> Zea mays

<400> 20

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
195 200 205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
210 215 220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225 230 235 240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr

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<210> 21
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<212> DNA
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<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (321)

<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99

Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147

Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195

Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243

Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly

80	85	90	
tct cag ctc ttt cct ctg aca agc aca acn gct acg cct gct gta cct	339		
Ser Gln Leu Phe Pro Leu Thr Ser Thr Thr Ala Thr Pro Ala Val Pro			
95 100 105 110			
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc	387		
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe			
115 120 125			
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act	435		
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr			
130 135 140			
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483		
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn			
145 150 155			
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa	531		
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu			
160 165 170			
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579		
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe			
175 180 185 190			
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627		
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile			
195 200 205			
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675		
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu			
210 215 220			
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723		
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala			
225 230 235			
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771		
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp			
240 245 250			
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819		
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp			
255 260 265 270			
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867		
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp			
275 280 285			
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915		
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe			
290 295 300			
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963		
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu			
305 310 315			


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cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt 1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser
    320                      325                      330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc 1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
    335                      340                      345                      350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag 1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
    355                      360                      365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
    370                      375                      380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc 1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
    385                      390                      395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
    400                      405                      410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
    415                      420                      425                      430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
    435                      440                      445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
    450                      455                      460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
    465                      470                      475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
    480                      485                      490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
    495                      500                      505                      510

aac gat ggg tct gtc ata tagatcggct gcgktktgcg 1576
Asn Asp Gly Ser Val Ile
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<210> 22

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<212> PRT

<213> Zea mays

<400> 22

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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
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Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
      35              40              45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50              55              60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65              70              75              80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
          85              90              95

Leu Phe Pro Leu Thr Ser Thr Thr Ala Thr Pro Ala Val Pro Val Gly
          100              105              110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
      115              120              125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130              135              140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145              150              155              160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
          165              170              175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
          180              185              190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
      195              200              205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
 210              215              220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225              230              235              240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
          245              250              255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
      260              265              270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
      275              280              285

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Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
 290 295 300
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
 305 310 315 320
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
 325 330 335
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
 385 390 395 400
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
 485 490 495
 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
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 Gly Ser Val Ile
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<210> 23

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>
 <221> variation
 <222> (267)
 <223> k = g or t; amino acid 86 = Ala.

<220>
 <221> variation
 <222> (1008)
 <223> y = c or t.

<220>
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 <222> (1368)
 <223> r = a or g; amino acid 453 = Pro.

<220>
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 <222> (1389)
 <223> h = a or c or t/u.

<220>
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 <222> (1578)
 <223> k = g or t.

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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
 65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
 80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe

115										120					125					
aac	agt	ggt	ata	aat	aag	ata	ttt	gtg	atg	agt	cag	ttc	aat	tct	act	435				
Asn	Ser	Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr					
130										135					140					
tcg	ctt	aac	cgc	cat	att	cat	cgt	aca	tac	ctt	gaa	ggc	ggg	atc	aac	483				
Ser	Leu	Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn					
145										150					155					
ttt	gct	gat	gga	tct	gta	cag	gta	tta	gcg	gct	aca	caa	atg	cct	gaa	531				
Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu					
160										165					170					
gag	cca	gct	gga	tgg	ttc	cag	ggt	aca	gca	gac	tct	atc	aga	aaa	ttt	579				
Glu	Pro	Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe					
175										180					185					190
atc	tgg	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627				
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile					
195										200					205					
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675				
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu					
210										215					220					
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723				
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala					
225										230					235					
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771				
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp					
240										245					250					
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggt	gct	gat	819				
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp					
255										260					265					270
ttg	aat	tct	atg	aga	gtt	gag	acc	aac	ttc	ctg	agc	tat	gct	ata	gat	867				
Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp					
275										280					285					
gat	gca	cag	aaa	tat	cca	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc	915				
Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe					
290										295					300					
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta	963				
Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu					
305										310					315					
cat	gac	ttt	gga	tct	gaa	atc	ctc	cca	aga	gct	gta	cta	gat	tay	agt	1011				
His	Asp	Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Tyr	Ser					
320										325					330					
gtg	cag	gca	tgc	att	ttt	acg	ggc	tat	tgg	gag	gat	gtt	gga	aca	atc	1059				
Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile					
335										340					345					350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag 1107
 Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
 355 360 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155
 Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
 370 375 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc 1203
 Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
 385 390 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
 Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
 400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
 415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
 435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac ath aag ata 1395
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Ile Lys Ile
 450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
 465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgktgtgcg 1576
 Asn Asp Gly Ser Val Ile
 515

<210> 24
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 <212> PRT
 <213> Zea mays

<400> 24

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile

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Gly	Gly	Arg	Lys	Gln	Glu	Lys	Ala	Leu	Arg	Asn	Arg	Cys	Phe	Gly	Gly
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Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala	Cys	Pro
	50					55					60				
Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	Ala	Asp
65					70					75					80
Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gln
				85					90					95	
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly
			100					105					110		
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser
		115					120					125			
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu
130							135					140			
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala
145						150					155				160
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro
				165					170					175	
Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp
			180					185					190		
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile
		195					200					205			
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln
	210					215					220				
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val
225						230					235				240
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr
				245					250					255	
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn
			260					265					270		
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala
		275					280						285		
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys
	290						295				300				
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp
305						310					315				320
Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Tyr	Ser	Val	Gln

325										330					335				
Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser				
			340						345					350					
Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	Phe	Asp				
		355					360					365							
Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys	Leu	Pro				
	370						375					380							
Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Ala	Phe	Ile	Ser	Asp				
385					390					395					400				
Gly	Cys	Leu	Leu	Arg	Glu	Cys	Asn	Ile	Glu	His	Ser	Val	Ile	Gly	Val				
				405					410					415					
Cys	Ser	Arg	Val	Ser	Ser	Gly	Cys	Glu	Leu	Lys	Asp	Ser	Val	Met	Met				
			420					425					430						
Gly	Ala	Asp	Ile	Tyr	Glu	Thr	Glu	Glu	Glu	Ala	Ser	Lys	Leu	Leu	Leu				
		435					440					445							
Ala	Gly	Lys	Val	Pro	Val	Gly	Ile	Gly	Arg	Asn	Ile	Lys	Ile	Arg	Asn				
	450					455					460								
Cys	Ile	Ile	Asp	Met	Asn	Ala	Arg	Ile	Gly	Lys	Asn	Val	Val	Ile	Thr				
465					470					475					480				
Asn	Ser	Lys	Gly	Ile	Gln	Glu	Ala	Asp	His	Pro	Glu	Glu	Gly	Tyr	Tyr				
			485					490						495					
Ile	Arg	Ser	Gly	Ile	Val	Val	Ile	Leu	Lys	Asn	Ala	Thr	Ile	Asn	Asp				
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Gly	Ser	Val	Ile																
		515																	

<210> 25

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (657)

<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

<400> 25

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His

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10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly
80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
115 120 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
130 135 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn

145	150	155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa			531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu			
160	165	170	
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt			579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe			
175	180	185	190
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att			627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile			
	195	200	205
gta atc ttg agt ggc gat cag ctt tat ccn atg aat tac atg gaa ctt			675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Pro Met Asn Tyr Met Glu Leu			
	210	215	220
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct			723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala			
	225	230	235
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat			771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp			
	240	245	250
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat			819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp			
	255	260	265
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat			867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp			
	275	280	285
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc			915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe			
	290	295	300
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta			963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu			
	305	310	315
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt			1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser			
	320	325	330
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc			1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile			
	335	340	345
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag			1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys			
	355	360	365
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc			1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys			

370	375	380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc			1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile			
385	390	395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att			1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile			
400	405	410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctg aag gac tcc gtg			1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val			
415	420	425	430
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta			1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu			
435	440	445	
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata			1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile			
450	455	460	
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg			1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val			
465	470	475	
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg			1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly			
480	485	490	
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc			1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile			
495	500	505	510
aac gat ggg tct gtc ata tagatcggct gcgktgtgcg			1576
Asn Asp Gly Ser Val Ile			
515			

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<211> 516

<212> PRT

<213> Zea mays

<400> 26

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Arg	Ser	Cys	Glu	Gly	Asp	Gly	Ile	Asp	Arg	Leu	Glu	Lys	Leu	Ser	Ile
			20					25					30		
Gly	Gly	Arg	Lys	Gln	Glu	Lys	Ala	Leu	Arg	Asn	Arg	Cys	Phe	Gly	Gly
			35				40					45			
Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala	Cys	Pro
	50					55					60				

Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	Ala	Asp	
65					70					75					80	
Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gln	
			85						90					95		
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly	
			100					105					110			
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser	
		115					120					125				
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu	
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Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala	
145					150					155					160	
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro	
			165						170					175		
Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp	
			180					185					190			
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile	
	195						200					205				
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Pro	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln	
	210					215					220					
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val	
225					230					235					240	
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr	
				245					250					255		
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn	
			260					265					270			
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala	
		275					280					285				
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys	
	290					295					300					
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp	
305					310					315					320	
Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Tyr	Ser	Val	Gln	
				325					330					335		
Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser	
			340					345					350			
Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	Phe	Asp	
		355					360					365				

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
 385 390 395 400
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
 485 490 495
 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
 500 505 510
 Gly Ser Val Ile
 515

<210> 27
 <211> 1576
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (10)..(1563)
 <223> Shrunk-2 gene revertant form, modified to be
 heat stable

<220>
 <221> variation
 <222> (267)
 <223> k = g or t; amino acid 86 = Ala.

<220>
 <221> variation
 <222> (540)
 <223> n = a or g or c or t/u, unknown, or other.

<220>
 <221> variation
 <222> (1008)
 <223> y = c or t.

<220>

<221> variation

<222> (1287)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

<400> 27

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His

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5

10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99

Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

15

20

25

30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147

Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe

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ggg ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195

Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala

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tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243

Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr

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gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly

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85

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tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339

Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro

95

100

105

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gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387

Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe

115

120

125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435

Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr

130

135

140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483

Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn

145

150

155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa	531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	
160 165 170	
gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
175 180 185 190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
210 215 220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
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Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser	
320 325 330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc	1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
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ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	
370 375 380	

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Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
      385              390              395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
      400              405              410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa tty aag gac tcc gtg 1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Phe Lys Asp Ser Val
415              420              425              430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
      435              440              445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
      450              455              460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
      465              470              475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
      480              485              490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
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aac gat ggg tct gtc ata tagatcggct gcgktgtgcg 1576
Asn Asp Gly Ser Val Ile
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<210> 28

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<213> Zea mays

<400> 28

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Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
      35              40              45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
      50              55              60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp

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Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly
			100					105					110		
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser
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Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu
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Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala
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Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro
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Val	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp
			180					185					190		
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile
		195					200					205			
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln
	210						215				220				
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val
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Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr
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Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn
			260					265					270		
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala
		275					280					285			
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys
	290					295					300				
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp
305					310					315					320
Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	His	Ser	Val	Gln
				325					330					335	
Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser
			340					345					350		
Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	Phe	Asp
		355					360					365			
Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys	Leu	Pro

370	375	380
Pro Thr Gln Leu Asp	Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp	
385	390	395 400
Gly Cys Leu Leu Arg	Glu Cys Asn Ile Glu His Ser Val Ile Gly Val	
	405	410 415
Cys Ser Arg Val Ser Ser Gly Cys Glu Phe Lys Asp Ser Val Met Met		
	420 425	430
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu		
	435 440	445
Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn		
	450 455	460
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr		
465	470	475 480
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr		
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Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp		
	500 505	510
Gly Ser Val Ile		
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 <213> Zea mays

<220>
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 <222> (10)..(1563)
 <223> Shrunk-2 gene revertant form, modified to be
 heat stable

<220>
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 <222> (267)
 <223> k = g or t; amino acid 86 = Ala.

<220>
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 <222> (981)
 <223> r = g or a.

<220>
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 <223> y = c or t.

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 <222> (1086)
 <223> n = a or g or c or t/u, unknown, or other.

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 <222> (1197)
 <223> n = a or g or c or t/u, unknown, or other.

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 <223> r = a or g; amino acid 453 = Pro.

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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
 65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Thr Gly
 80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
 115 120 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
 130 135 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483

Ser	Leu	Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn		
		145					150					155					
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Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu		
	160					165				170							
gag	cca	gct	gga	tgg	ttc	cag	ggt	aca	gca	gac	tct	atc	aga	aaa	ttt	579	
Glu	Pro	Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe		
175					180				185					190			
atc	tgg	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627	
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile		
				195				200						205			
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675	
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu		
			210					215					220				
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723	
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala		
		225					230					235					
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771	
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp		
	240					245				250							
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggt	gct	gat	819	
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp		
255					260				265						270		
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Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp		
				275				280						285			
gat	gca	cag	aaa	tat	cca	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc	915	
Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe		
			290					295					300				
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta	963	
Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu		
		305					310					315					
cat	gac	ttt	gga	tct	aar	atc	ctc	cca	aga	gct	gta	cta	gat	cay	agt	1011	
His	Asp	Phe	Gly	Ser	Lys	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	His	Ser		
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Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile		
335					340				345					350			
aaa	tca	ttc	ttt	gat	gca	aac	ttg	gtt	ctc	act	gag	cag	cct	tcc	aag	1107	
Lys	Ser	Phe	Phe	Asp	Ala	Asn	Leu	Val	Leu	Thr	Glu	Gln	Pro	Ser	Lys		
				355				360					365				
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385	390	395	
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Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile			
400	405	410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg			1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val			
415	420	425	430
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta			1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu			
435	440	445	
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata			1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile			
450	455	460	
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg			1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val			
465	470	475	
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg			1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly			
480	485	490	
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc			1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile			
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<213> Zea mays

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Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95
 Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175
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 180 185 190
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
 195 200 205
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
 210 215 220
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
 225 230 235 240
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
 245 250 255
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
 260 265 270
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
 275 280 285
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
 290 295 300
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
 305 310 315 320
 Phe Gly Ser Lys Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
 325 330 335
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350
 Phe Phe Asp Ala Asn Leu Val Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
 385 390 395 400
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
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<220>
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 heat stable

<220>
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 <223> k = g or t; amino acid 86 = Ala.

<220>
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<220>
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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His

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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99

Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

15

20

25

30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147

Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe

35

40

45

ggg ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195

Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala

50

55

60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243

Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr

65

70

75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly

80

85

90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339

Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro

95

100

105

110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387

Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe

115

120

125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435

Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr

130

135

140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483

Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn

145

150

155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531

Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu

160

165

170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579

Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe

175

180

185

190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627

Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile

195										200					205					
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675				
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu					
210					215					220										
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723				
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala					
225					230					235										
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771				
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp					
240					245					250										
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggt	gct	gat	819				
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp					
255					260					265					270					
ttg	aat	tct	atg	aga	gtt	gag	acc	aac	ttc	ctg	agc	tat	gct	ata	gat	867				
Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp					
275					280					285										
gat	gca	cag	aaa	tat	cca	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc	915				
Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe					
290					295					300										
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta	963				
Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu					
305					310					315										
cat	gac	ttt	gga	tct	gaa	atc	ctc	cca	aga	gct	gta	cta	gat	tty	agt	1011				
His	Asp	Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Phe	Ser					
320					325					330										
gtg	cag	gca	tgc	att	ttt	acg	ggc	tat	tgg	gag	gat	gtt	gga	aca	atc	1059				
Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile					
335					340					345					350					
aaa	tca	ttc	ttt	gat	gca	aac	ttg	gcc	ctc	act	gag	cag	cct	tcc	aag	1107				
Lys	Ser	Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys					
355					360					365										
ttt	gat	ttt	tac	gat	cca	aaa	aca	cct	ttc	ttc	act	gca	ccc	cga	tgc	1155				
Phe	Asp	Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys					
370					375					380										
ttg	cct	ccg	acg	caa	ttg	gac	aag	tgc	aag	atg	aaa	tat	gca	ttt	atc	1203				
Leu	Pro	Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Ala	Phe	Ile					
385					390					395										
tca	gat	ggt	tgc	tta	ctg	aga	gaa	tgc	aac	atc	gag	cat	tct	gtg	att	1251				
Ser	Asp	Gly	Cys	Leu	Leu	Arg	Glu	Cys	Asn	Ile	Glu	His	Ser	Val	Ile					
400					405					410										
gga	gtc	tgc	tca	cgt	gtc	agc	tct	gga	tgt	gaa	ctc	aag	gac	tcc	gtg	1299				
Gly	Val	Cys	Ser	Arg	Val	Ser	Ser	Gly	Cys	Glu	Leu	Lys	Asp	Ser	Val					
415					420					425					430					

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atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
      435              440              445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
      450              455              460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
      465              470              475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
      480              485              490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
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aac gat ggg tct gtc ata tagatcggct gcgktkgcg 1576
Asn Asp Gly Ser Val Ile
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<210> 32

<211> 516

<212> PRT

<213> Zea mays

<400> 32

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
      20              25              30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
      35              40              45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
      50              55              60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
      65              70              75              80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
      85              90              95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
      100              105              110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
      115              120              125

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Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu	130	135	140
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala	145	150	155
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro	165	170	175
Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp	180	185	190
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile	195	200	205
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln	210	215	220
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val	225	230	235
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr	245	250	255
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn	260	265	270
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala	275	280	285
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys	290	295	300
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp	305	310	315
Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Phe	Ser	Val	Gln	325	330	335
Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser	340	345	350
Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	Phe	Asp	355	360	365
Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys	Leu	Pro	370	375	380
Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Ala	Phe	Ile	Ser	Asp	385	390	395
Gly	Cys	Leu	Leu	Arg	Glu	Cys	Asn	Ile	Glu	His	Ser	Val	Ile	Gly	Val	405	410	415
Cys	Ser	Arg	Val	Ser	Ser	Gly	Cys	Glu	Leu	Lys	Asp	Ser	Val	Met	Met	420	425	430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
 485 490 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
 500 505 510

Gly Ser Val Ile
 515

<210> 33
 <211> 1576
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (10)..(1563)
 <223> Shrunk-2 gene revertant form, modified to be
 heat stable

<220>
 <221> variation
 <222> (267)
 <223> k = g or t; amino acid 86 = Ala.

<220>
 <221> variation
 <222> (1008)
 <223> y = c or t.

<220>
 <221> variation
 <222> (1368)
 <223> r = a or g; amino acid 453 = Pro.

<220>
 <221> variation
 <222> (1578)
 <223> k = g or t.

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 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
 1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

15	20	25	30	
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt				147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe	35	40	45	
ggg ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct				195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala	50	55	60	
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat				243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr	65	70	75	
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga				291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly	80	85	90	
tct cag ctg ttt cct ctg aca agc aca aga gct acg cct gct gta cct				339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro	95	100	105	110
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc				387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe	115	120	125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act				435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	130	135	140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac				483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	145	150	155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa				531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	160	165	170	
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt				579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	175	180	185	190
atc tgg gta ctg gag gat tat tac agt cac aaa tcc att gac aac att				627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	195	200	205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt				675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	210	215	220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct				723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	225	230	235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat				771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	240	245	250	

cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat atg agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Met Ser	
320 325 330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc	1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
355 360 365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	
370 375 380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc	1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile	
385 390 395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att	1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile	
400 405 410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg	1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val	
415 420 425 430	
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta	1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu	
435 440 445	
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata	1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile	
450 455 460	
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg	1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val	
465 470 475	

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgktgcg 1576
 Asn Asp Gly Ser Val Ile
 515

<210> 34
 <211> 516
 <212> PRT
 <213> Zea mays

<400> 34

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
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Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile

195	200	205
Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln		
210	215	220
Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val		
225	230	235 240
Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr		
	245	250 255
Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn		
	260	265 270
Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala		
	275	280 285
Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys		
	290	295 300
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp		
305	310	315 320
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Met Ser Val Gln		
	325	330 335
Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser		
	340	345 350
Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp		
	355	360 365
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro		
	370	375 380
Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp		
385	390	395 400
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val		
	405	410 415
Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met		
	420	425 430
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu		
	435	440 445
Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn		
	450	455 460
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr		
465	470	475 480
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr		
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Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp		

500

505

510

Gly Ser Val Ile
515

<210> 35
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (540)
<223> n = a or g or c or t/u, unknown, or other.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

<220>
<221> variation
<222> (1578)
<223> k = g or t.

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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala

50										55					60					
tgt	cct	gaa	act	ctt	cat	tct	caa	aca	cag	tcc	tct	agg	aaa	aat	tat	243				
Cys	Pro	Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr					
65			70			75														
gct	gat	gca	aac	cgt	gta	tct	gck	atc	att	ttg	ggc	gga	ggc	act	gga	291				
Ala	Asp	Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly					
80			85			90														
tct	cag	ctc	ttt	cct	ctg	aca	agc	aca	aga	gct	acg	cct	gct	gta	cct	339				
Ser	Gln	Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro					
95			100			105						110								
gtt	gga	gga	tgt	tac	agg	ctt	att	gat	atc	cct	atg	agt	aac	tgc	ttc	387				
Val	Gly	Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe					
			115			120						125								
aac	agt	ggt	ata	aat	aag	ata	ttt	gtg	atg	agt	cag	ttc	aat	tct	act	435				
Asn	Ser	Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr					
130			135			140														
tcg	ctt	aac	cgc	cat	att	cat	cgt	aca	tac	ctt	gaa	ggc	ggg	atc	aac	483				
Ser	Leu	Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn					
145			150			155														
ttt	gct	gat	gga	tct	gta	cag	gta	tta	gcg	gct	aca	caa	atg	cct	gaa	531				
Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu					
160			165			170														
gag	cca	gtg	gga	tgg	ttc	cag	ggt	aca	gca	gac	tct	atc	aga	aaa	ttt	579				
Glu	Pro	Val	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe					
175			180			185						190								
atc	tgg	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627				
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile					
			195			200						205								
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675				
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu					
210			215			220														
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723				
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala					
225			230			235														
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771				
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp					
240			245			250														
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggt	gct	gat	819				
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp					
255			260			265						270								
ttg	aat	tct	atg	aga	gtt	gag	acc	aac	ttc	ctg	agc	tat	gct	ata	gat	867				
Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp					

275										280					285					
gat	gca	cag	aaa	tat	cca	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc	915				
Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe					
			290				295				300									
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta	963				
Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu					
			305				310				315									
cat	gac	ttt	gga	tct	gaa	atc	ctc	cca	aga	gct	gta	cta	gat	tay	agt	1011				
His	Asp	Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Tyr	Ser					
			320				325				330									
gtg	cag	gca	tgc	att	ttt	acg	ggc	tat	tgg	gag	gat	gtt	gga	aca	atc	1059				
Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile					
335				340				345				350								
aaa	tca	ttc	ttt	gat	gca	aac	ttg	gcc	ctc	act	gag	cag	cct	tcc	aag	1107				
Lys	Ser	Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys					
			355				360				365									
ttt	gat	ttt	tac	gat	cca	aaa	aca	cct	ttc	ttc	act	gca	ccc	cga	tgc	1155				
Phe	Asp	Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys					
			370				375				380									
ttg	cct	ccg	acg	caa	ttg	gac	aag	tgc	aag	atg	aaa	tat	gca	ttt	atc	1203				
Leu	Pro	Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Ala	Phe	Ile					
			385				390				395									
tca	gat	ggg	tgc	tta	ctg	aga	gaa	tgc	aac	atc	gag	cat	tct	gtg	att	1251				
Ser	Asp	Gly	Cys	Leu	Leu	Arg	Glu	Cys	Asn	Ile	Glu	His	Ser	Val	Ile					
			400				405				410									
gga	gtc	tgc	tca	cgt	gtc	agc	tct	gga	tgt	gaa	ctc	aag	gac	tcc	gtg	1299				
Gly	Val	Cys	Ser	Arg	Val	Ser	Ser	Gly	Cys	Glu	Leu	Lys	Asp	Ser	Val					
415				420				425				430								
atg	atg	gga	gcg	gac	atc	tat	gaa	act	gaa	gaa	gaa	gct	tca	aag	cta	1347				
Met	Met	Gly	Ala	Asp	Ile	Tyr	Glu	Thr	Glu	Glu	Glu	Ala	Ser	Lys	Leu					
			435				440				445									
ctg	tta	gct	ggg	aag	gtc	ccr	gtt	gga	ata	gga	agg	aac	aca	aag	ata	1395				
Leu	Leu	Ala	Gly	Lys	Val	Pro	Val	Gly	Ile	Gly	Arg	Asn	Thr	Lys	Ile					
			450				455				460									
agg	aac	tgt	atc	att	gac	atg	aat	gct	agg	att	ggg	aag	aac	gtg	gtg	1443				
Arg	Asn	Cys	Ile	Ile	Asp	Met	Asn	Ala	Arg	Ile	Gly	Lys	Asn	Val	Val					
			465				470				475									
atc	aca	aac	agt	aag	ggc	atc	caa	gag	gct	gat	cac	ccg	gaa	gaa	ggg	1491				
Ile	Thr	Asn	Ser	Lys	Gly	Ile	Gln	Glu	Ala	Asp	His	Pro	Glu	Glu	Gly					
			480				485				490									
tac	tac	ata	agg	tct	gga	atc	gtg	gtg	atc	ctg	aag	aat	gca	acc	atc	1539				
Tyr	Tyr	Ile	Arg	Ser	Gly	Ile	Val	Val	Ile	Leu	Lys	Asn	Ala	Thr	Ile					
495				500				505				510								

aac gat ggg tct gtc ata tagatcggct gcgktgtgcg
 Asn Asp Gly Ser Val Ile
 515

1576

<210> 36
 <211> 516
 <212> PRT
 <213> Zea mays

<400> 36

Met	Gln	Phe	Ala	Leu	Ala	Leu	Asp	Thr	Asn	Ser	Gly	Pro	His	Gln	Ile	1	5	10	15
Arg	Ser	Cys	Glu	Gly	Asp	Gly	Ile	Asp	Arg	Leu	Glu	Lys	Leu	Ser	Ile	20	25	30	
Gly	Gly	Arg	Lys	Gln	Glu	Lys	Ala	Leu	Arg	Asn	Arg	Cys	Phe	Gly	Gly	35	40	45	
Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala	Cys	Pro	50	55	60	
Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	Ala	Asp	65	70	75	80
Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gln	85	90	95	
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly	100	105	110	
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser	115	120	125	
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu	130	135	140	
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala	145	150	155	160
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro	165	170	175	
Val	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp	180	185	190	
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile	195	200	205	
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln	210	215	220	
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val	225	230	235	240

<210> 37

<211> 1576
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (10)..(1563)
 <223> Shrunk-2 gene revertant form, modified to be
 heat stable

<220>
 <221> variation
 <222> (267)
 <223> k = g or t; amino acid 86 = Ala.

<220>
 <221> variation
 <222> (1008)
 <223> y = c or t.

<220>
 <221> variation
 <222> (1197)
 <223> n = a or g or c or t/u, unknown, or other.

<220>
 <221> variation
 <222> (1368)
 <223> r = a or g; amino acid 453 = Pro.

<220>
 <221> variation
 <222> (1578)
 <223> k = g or t.

<400> 37
 ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
 1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
 65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291

Ala	Asp	Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly		
80						85					90						
tct	cag	ctc	ttt	cct	ctg	aca	agc	aca	aga	gct	acg	cct	gct	gta	cct	339	
Ser	Gln	Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro		
95					100					105					110		
gtt	gga	gga	tgt	tac	agg	ctt	att	gat	atc	cct	atg	agt	aac	tgc	ttc	387	
Val	Gly	Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe		
				115					120					125			
aac	agt	ggt	ata	aat	aag	ata	ttt	gtg	atg	agt	cag	ttc	aat	tct	act	435	
Asn	Ser	Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr		
			130					135					140				
tcg	ctt	aac	cgc	cat	att	cat	cgt	aca	tac	ctt	gaa	ggc	ggg	atc	aac	483	
Ser	Leu	Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn		
		145					150					155					
ttt	gct	gat	gga	tct	gta	cag	gta	tta	gcg	gct	aca	caa	atg	cct	gaa	531	
Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu		
	160					165					170						
gag	cca	gct	gga	tgg	ttc	cag	ggt	aca	gca	gac	tct	atc	aga	aaa	ttt	579	
Glu	Pro	Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe		
175					180					185					190		
atc	tgg	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627	
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile		
				195					200					205			
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675	
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu		
			210					215					220				
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723	
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala		
		225					230					235					
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771	
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp		
	240					245					250						
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggt	gct	gat	819	
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp		
	255				260					265					270		
ttg	aat	tct	atg	aga	gtt	gag	acc	aac	ttc	ctg	agc	tat	gct	ata	gat	867	
Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp		
				275					280					285			
gat	gca	cag	aaa	tat	cca	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc	915	
Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe		
			290					295					300				
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta	963	

Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu		
		305					310					315					
cat	gac	ttt	gga	tct	gaa	atc	ctc	cca	aga	gct	gta	cta	gat	tay	agt	1011	
His	Asp	Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Tyr	Ser		
	320					325					330						
gtg	cag	gca	tgc	att	ttt	acg	ggc	tat	tgg	gag	gat	gtt	gga	aca	atc	1059	
Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile		
335					340					345					350		
aaa	tca	ttc	ttt	gat	gca	aac	ttg	gcc	ctc	act	gag	cag	cct	tcc	aag	1107	
Lys	Ser	Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys		
				355					360						365		
ttt	gat	ttt	tac	gat	cca	aaa	aca	cct	ttc	ttc	act	gca	ccc	cga	tgc	1155	
Phe	Asp	Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys		
			370					375						380			
ttg	cct	ccg	acg	caa	ttg	gac	aag	tgc	aag	atg	aaa	tat	gtt	ttt	atc	1203	
Leu	Pro	Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Val	Phe	Ile		
		385					390					395					
tca	gat	ggt	tgc	tta	ctg	aga	gaa	tgc	aac	atc	gag	cat	tct	gtg	att	1251	
Ser	Asp	Gly	Cys	Leu	Leu	Arg	Glu	Cys	Asn	Ile	Glu	His	Ser	Val	Ile		
	400					405					410						
gga	gtc	tgc	tca	cgt	gtc	agc	tct	gga	tgt	gaa	ctc	aag	gac	tcc	gtg	1299	
Gly	Val	Cys	Ser	Arg	Val	Ser	Ser	Gly	Cys	Glu	Leu	Lys	Asp	Ser	Val		
415					420					425					430		
atg	atg	gga	gcg	gac	atc	tat	gaa	act	gaa	gaa	gaa	gct	tca	aag	cta	1347	
Met	Met	Gly	Ala	Asp	Ile	Tyr	Glu	Thr	Glu	Glu	Glu	Ala	Ser	Lys	Leu		
				435					440					445			
ctg	tta	gct	ggg	aag	gtc	ccr	gtt	gga	ata	gga	agg	aac	aca	aag	ata	1395	
Leu	Leu	Ala	Gly	Lys	Val	Pro	Val	Gly	Ile	Gly	Arg	Asn	Thr	Lys	Ile		
			450					455						460			
agg	aac	tgt	atc	att	gac	atg	aat	gct	agg	att	ggg	aag	aac	gtg	gtg	1443	
Arg	Asn	Cys	Ile	Ile	Asp	Met	Asn	Ala	Arg	Ile	Gly	Lys	Asn	Val	Val		
		465					470					475					
atc	aca	aac	agt	aag	ggc	atc	caa	gag	gct	gat	cac	ccg	gaa	gaa	ggg	1491	
Ile	Thr	Asn	Ser	Lys	Gly	Ile	Gln	Glu	Ala	Asp	His	Pro	Glu	Glu	Gly		
	480					485					490						
tac	tac	ata	agg	tct	gga	atc	gtg	gtg	atc	ctg	aag	aat	gca	acc	atc	1539	
Tyr	Tyr	Ile	Arg	Ser	Gly	Ile	Val	Val	Ile	Leu	Lys	Asn	Ala	Thr	Ile		
495					500					505					510		
aac	gat	ggg	tct	gtc	ata	tagatcggct	gcgktgtgcg									1576	
Asn	Asp	Gly	Ser	Val	Ile												
				515													

<210> 38

<211> 516
 <212> PRT
 <213> Zea mays

<400> 38

Met	Gln	Phe	Ala	Leu	Ala	Leu	Asp	Thr	Asn	Ser	Gly	Pro	His	Gln	Ile	1	5	10	15
Arg	Ser	Cys	Glu	Gly	Asp	Gly	Ile	Asp	Arg	Leu	Glu	Lys	Leu	Ser	Ile	20	25	30	
Gly	Gly	Arg	Lys	Gln	Glu	Lys	Ala	Leu	Arg	Asn	Arg	Cys	Phe	Gly	Gly	35	40	45	
Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala	Cys	Pro	50	55	60	
Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	Ala	Asp	65	70	75	80
Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gln	85	90	95	
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly	100	105	110	
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser	115	120	125	
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu	130	135	140	
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala	145	150	155	160
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro	165	170	175	
Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp	180	185	190	
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile	195	200	205	
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln	210	215	220	
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val	225	230	235	240
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr	245	250	255	
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn	260	265	270	

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
 275 280 285
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
 290 295 300
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
 305 310 315 320
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
 325 330 335
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
 385 390 395 400
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
 485 490 495
 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
 500 505 510
 Gly Ser Val Ile
 515

<210> 39

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (540)

<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1197)

<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

<400> 39

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct	339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro	
95 100 105 110	
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc	387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe	
115 120 125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act	435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	
130 135 140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	
145 150 155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa	531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	
160 165 170	
gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
175 180 185 190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
210 215 220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	

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cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt 1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser
    320                      325                      330

gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc 1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
    335                      340                      345                      350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag 1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
    355                      360                      365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
    370                      375                      380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc 1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
    385                      390                      395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
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gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
    415                      420                      425                      430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
    435                      440                      445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
    450                      455                      460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
    465                      470                      475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
    480                      485                      490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
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aac gat ggg tct gtc ata tagatcggct gcgtktgcg 1576
Asn Asp Gly Ser Val Ile
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<210> 40

<211> 516

<212> PRT

<213> Zea mays

<400> 40

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Arg  Ser  Cys  Glu  Gly  Asp  Gly  Ile  Asp  Arg  Leu  Glu  Lys  Leu  Ser  Ile
      20              25              30

Gly  Gly  Arg  Lys  Gln  Glu  Lys  Ala  Leu  Arg  Asn  Arg  Cys  Phe  Gly  Gly
      35              40              45

Arg  Val  Ala  Ala  Thr  Thr  Gln  Cys  Ile  Leu  Thr  Ser  Asp  Ala  Cys  Pro
      50              55              60

Glu  Thr  Leu  His  Ser  Gln  Thr  Gln  Ser  Ser  Arg  Lys  Asn  Tyr  Ala  Asp
      65              70              75              80

Ala  Asn  Arg  Val  Ser  Ala  Ile  Ile  Leu  Gly  Gly  Gly  Thr  Gly  Ser  Gln
      85              90              95

Leu  Phe  Pro  Leu  Thr  Ser  Thr  Arg  Ala  Thr  Pro  Ala  Val  Pro  Val  Gly
      100              105              110

Gly  Cys  Tyr  Arg  Leu  Ile  Asp  Ile  Pro  Met  Ser  Asn  Cys  Phe  Asn  Ser
      115              120              125

Gly  Ile  Asn  Lys  Ile  Phe  Val  Met  Ser  Gln  Phe  Asn  Ser  Thr  Ser  Leu
      130              135              140

Asn  Arg  His  Ile  His  Arg  Thr  Tyr  Leu  Glu  Gly  Gly  Ile  Asn  Phe  Ala
      145              150              155              160

Asp  Gly  Ser  Val  Gln  Val  Leu  Ala  Ala  Thr  Gln  Met  Pro  Glu  Glu  Pro
      165              170              175

Val  Gly  Trp  Phe  Gln  Gly  Thr  Ala  Asp  Ser  Ile  Arg  Lys  Phe  Ile  Trp
      180              185              190

Val  Leu  Glu  Asp  Tyr  Tyr  Ser  His  Lys  Ser  Ile  Asp  Asn  Ile  Val  Ile
      195              200              205

Leu  Ser  Gly  Asp  Gln  Leu  Tyr  Arg  Met  Asn  Tyr  Met  Glu  Leu  Val  Gln
      210              215              220

Lys  His  Val  Glu  Asp  Asp  Ala  Asp  Ile  Thr  Ile  Ser  Cys  Ala  Pro  Val
      225              230              235              240

Asp  Glu  Ser  Arg  Ala  Ser  Lys  Asn  Gly  Leu  Val  Lys  Ile  Asp  His  Thr
      245              250              255

Gly  Arg  Val  Leu  Gln  Phe  Phe  Glu  Lys  Pro  Lys  Gly  Ala  Asp  Leu  Asn
      260              265              270

Ser  Met  Arg  Val  Glu  Thr  Asn  Phe  Leu  Ser  Tyr  Ala  Ile  Asp  Asp  Ala
      275              280              285

Gln  Lys  Tyr  Pro  Tyr  Leu  Ala  Ser  Met  Gly  Ile  Tyr  Val  Phe  Lys  Lys

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290	295	300
Asp Ala Leu Leu Asp	Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp	
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Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln		
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Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser		
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Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp		
	355	360 365
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro		
	370	375 380
Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp		
	385	390 395 400
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val		
	405	410 415
Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met		
	420	425 430
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu		
	435	440 445
Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn		
	450	455 460
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr		
	465	470 475 480
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr		
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Gly Ser Val Ile		
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<210> 41

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>

<221> variation
 <222> (267)
 <223> k = g or t; amino acid 86 = Ala.

 <220>
 <221> variation
 <222> (540)
 <223> n = a or g or c or t/u, unknown, or other.

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 <222> (1008)
 <223> y = c or t.

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 <222> (1197)
 <223> n = a or g or c or t/u, unknown, or other.

 <220>
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 <222> (1368)
 <223> r = a or g; amino acid 453 = Pro.

 <220>
 <221> variation
 <222> (1578)
 <223> k = g or t.

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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
 65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
 80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc	387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe	
115 120 125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act	435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	
130 135 140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	
145 150 155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa	531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	
160 165 170	
gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
175 180 185 190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
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Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
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Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser	
320 325 330	

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 Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile
 335 340 345 350

aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag 1107
 Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
 355 360 365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155
 Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
 370 375 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc 1203
 Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
 385 390 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
 Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
 400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
 415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
 435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
 450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
 465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
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<210> 42

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<212> PRT

<213> Zea mays

<400> 42

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Gly	Gly	Arg	Lys	Gln	Glu	Lys	Ala	Leu	Arg	Asn	Arg	Cys	Phe	Gly	Gly	35	40	45	
Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala	Cys	Pro	50	55	60	
Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	Ala	Asp	65	70	75	80
Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gln	85	90	95	
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly	100	105	110	
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser	115	120	125	
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu	130	135	140	
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala	145	150	155	160
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro	165	170	175	
Val	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp	180	185	190	
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile	195	200	205	
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln	210	215	220	
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val	225	230	235	240
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr	245	250	255	
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn	260	265	270	
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala	275	280	285	
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys	290	295	300	

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
 305 310 315 320
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
 325 330 335
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
 385 390 395 400
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
 485 490 495
 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
 500 505 510
 Gly Ser Val Ile
 515